

SEQUENCE LISTING

<110> Maliszewski, Charles R.
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Gimpel, Steven D.

<120> Inhibitors of Platelet Activation and Recruitment

<130> 2879-US

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<150> US 60/104,585

<151> 1998-10-16

<150> US 60/107,466

<151> 1998-11-06

<150> US 60/149,010

<151> 1999-08-13

<150> PCT/US99/22955

<151> 1999-10-13

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<170> PatentIn Ver. 2.0

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<212> DNA

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<222> (67)..(1596)

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Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
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His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	
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gtt	cag	aaa	gta	aat	gaa	ata	ggc	att	tac	ctg	act	gat	tgc	atg	gaa	396
Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	
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Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	
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Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	
			130					135					140			
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Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	
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Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	
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Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	
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gaa	acc	ttt	gga	gct	ttg	gac	ctt	ggg	gga	gcc	tct	aca	caa	gtc	act	732
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Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	
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Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	
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Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	
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Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	
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Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	
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Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	
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Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	
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Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	
415					420					425					430	
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1404
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	
				435				440						445		
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1452
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	
			450					455					460			
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Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val	
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ttc	ctc	atg	gtt	cta	ttc	tcc	ctg	gtc	ctt	ttc	aca	gtg	gcc	atc	ata	1548
Phe	Leu	Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile	
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 35 40 45
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
 100 105 110
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
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 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
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 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
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 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
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 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
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 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
 225 230 235 240
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
 245 250 255
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
 260 265 270

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Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile		
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Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln		
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225					230					235					240		
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Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
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Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion
construct of human CD39

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Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60

Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	
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Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	
			85						90					95		
Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	
		100						105					110			
Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	
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Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	
	130					135					140					
Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	
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Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	
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Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	
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Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	
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Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	
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Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	
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Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	
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Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	
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Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	
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Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	
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Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	
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Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
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Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion
construct of human CD39

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<221> CDS

<222> (1)..(1362)

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Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp	
20 25 30	

gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa	144
Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu	
35 40 45	

aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt	192
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val	
50 55 60	

aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc	240
Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly	
65 70 75 80	

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg	288
Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg	
85 90 95	
tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg	336
Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met	
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cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat	384
Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp	
115 120 125	
gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc	432
Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala	
130 135 140	
agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc	480
Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile	
145 150 155 160	
aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata	528
Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile	
165 170 175	
gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt	576
Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu	
180 185 190	
ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc	624
Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile	
195 200 205	
gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac	672
Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr	
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Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu	
225 230 235 240	
tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc	768
Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu	
245 250 255	
agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt	816
Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser	
260 265 270	
gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca	864
Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro	
275 280 285	
ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat	912
Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His	
290 295 300	

caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag	960
Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln	
305 310 315 320	
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Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly	
325 330 335	
gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca	1056
Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser	
340 345 350	
gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt	1104
Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys	
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gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag	1152
Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu	
370 375 380	
aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc	1200
Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu	
385 390 395 400	
ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat	1248
Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His	
405 410 415	
ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac	1296
Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr	
420 425 430	
atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca	1344
Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr	
435 440 445	
cct ctc tcc cac tcc acc taa	1365
Pro Leu Ser His Ser Thr	
450	

<210> 6

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 6

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	Glu	35	40	45
Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	Val	50	55	60
Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	65	70	75
Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	85	90	95
Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	100	105	110
Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	115	120	125
Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	130	135	140
Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	145	150	155
Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	165	170	175
Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	180	185	190
Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	195	200	205
Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	210	215	220
Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	225	230	235
Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	245	250	255
Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	260	265	270
Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	275	280	285
Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	290	295	300
Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	305	310	315
Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	325	330	335

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
355 360 365

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
370 375 380

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
385 390 395 400

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
405 410 415

Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
420 425 430

Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
435 440 445

Pro Leu Ser His Ser Thr
450

<210> 7

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>

<221> CDS

<222> (1)..(1434)

<400> 7

atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta	48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu	
1 5 10 15	
agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag	96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys	
20 25 30	
aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac	144
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn	
35 40 45	
gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta	192
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu	
50 55 60	
tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg	240
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val	
65 70 75 80	

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt	288
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe	
85 90 95	
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa	336
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu	
100 105 110	
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	384
Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val	
115 120 125	
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	432
Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	
130 135 140	
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	480
Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	
145 150 155 160	
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	528
Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	
165 170 175	
ggg gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	576
Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	
180 185 190	
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	624
Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	
195 200 205	
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	672
Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr	
210 215 220	
ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa	720
Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln	
225 230 235 240	
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg	768
Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu	
245 250 255	
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att	816
Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile	
260 265 270	
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga	864
Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly	
275 280 285	
tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc	912
Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr	
290 295 300	

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aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 960
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
305 310 315 320

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1008
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
325 330 335

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1056
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1104
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1152
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1200
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
385 390 395 400

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1248
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
405 410 415

tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1296
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr
420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1344
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1392
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
450 455 460

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc taa 1437
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

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<210> 8
<211> 478
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Fusion
        construct of human CD39

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<400> 8
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
  1             5             10             15

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Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
 35 40 45
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 50 55 60
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75 80
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 85 90 95
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 100 105 110
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
 115 120 125
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
 130 135 140
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
 145 150 155 160
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
 165 170 175
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
 180 185 190
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
 195 200 205
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235 240
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 245 250 255
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 260 265 270
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
 305 310 315 320

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
450 455 460

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser
20

<210> 10

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 11
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 11
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
35 40

<210> 12
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 12
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
20 25

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 13
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
20 25 30

<210> 14
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 14
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctccac gagcccc 87

<210> 15
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 15
 gatcggggct cgtgggagag aggtgtggac aatgggttgc cagctgggat catgttggtc 60
 aggttcagca tgtagcccaa agtccag 87

<210> 16
 <211> 740
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (42)..(737)

<400> 16
 cggtagcgcg agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56
 Glu Pro Arg Ser Cys
 1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
 10 15 20

gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 152
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 25 30 35

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 200
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 40 45 50

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg	248
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	
55 60 65	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac	296
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	
70 75 80 85	
cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc	344
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
90 95 100	
aag gac tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atg	392
Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Met	
105 110 115	
cag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg	440
Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	
120 125 130	
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc	488
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser	
135 140 145	
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agg cac atc gcc gtg gag	536
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile Ala Val Glu	
150 155 160 165	
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	584
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	
170 175 180	
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg	632
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	
185 190 195	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg	680
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	
200 205 210	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct	728
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	
215 220 225	
ccg ggt aaa tga	740
Pro Gly Lys	
230	

<210> 17
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 17
 Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 18

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18

ctttccatcc tgagcaac

18

<210> 19

<211> 36

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20
<211> 24
<212> PRT
<213> Mus sp.

<400> 20
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser
20

<210> 21
<211> 46
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21
ctagttcttg agactacaaa gatgacgatg acaaaaccca gaacaa

46

<210> 22
<211> 46
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22
agctttgttc tgggttttgc catcgatcatc tttgtagtct ccagaa

46

<210> 23
<211> 89
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctcccac tccacctaa 89

<210> 24
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 24
 ggccttaggt ggagtgggag agaggtgtgg acaatgggtg ctcagctggg atcatgttgg 60
 tcaggttcag catgtagccc aaagtccag 89

<210> 25
 <211> 1464
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1461)

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 25
 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15
 agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30
 aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa 144
 Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
 35 40 45
 acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg 192
 Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
 50 55 60
 gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca 240
 Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
 65 70 75 80

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg	288
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg	
85 90 95	
gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata	336
Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile	
100 105 110	
ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca	384
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro	
115 120 125	
agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc	432
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly	
130 135 140	
atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg	480
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu	
145 150 155 160	
gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt	528
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly	
165 170 175	
gcc agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act	576
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr	
180 185 190	
atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc	624
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser	
195 200 205	
ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac	672
Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp	
210 215 220	
ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act	720
Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr	
225 230 235 240	
atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac	768
Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp	
245 250 255	
tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca	816
Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala	
260 265 270	
ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att	864
Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile	
275 280 285	
ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta	912
Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val	
290 295 300	

agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt	960
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu	
305 310 315 320	
cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc	1008
Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys	
325 330 335	
cat caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc	1056
His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser	
340 345 350	
cag tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt	1104
Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe	
355 360 365	
ggg gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca	1152
Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr	
370 375 380	
tca gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc	1200
Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe	
385 390 395 400	
tgt gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag	1248
Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys	
405 410 415	
gag aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc	1296
Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser	
420 425 430	
ctc ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc	1344
Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile	
435 440 445	
cat ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc	1392
His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly	
450 455 460	
tac atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc	1440
Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser	
465 470 475 480	
aca cct ctc tcc cac tcc acc taa	1464
Thr Pro Leu Ser His Ser Thr	
485	

<210> 26

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 26

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
1				5					10					15	
Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys
			20					25					30		
Lys	Thr	Gln	Leu	Thr	Ser	Ser	Gly	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
		35					40				45				
Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	Tyr	Gly	Ile	Val	Leu
	50					55				60					
Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala
65					70					75					80
Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg
			85						90					95	
Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile
			100					105					110		
Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro
	115						120					125			
Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly
	130					135					140				
Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu
145					150					155					160
Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly
			165					170						175	
Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr
		180					185						190		
Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser
	195					200						205			
Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp
	210					215					220				
Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr
225					230					235				240	
Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp
			245					250					255		
Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala
	260						265						270		
Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile
	275					280						285			
Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val
290						295					300				

Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	65	70	75	80
Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	85	90	95	
Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	100	105	110	
Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	115	120	125	
Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	130	135	140	
Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	145	150	155	160
Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	165	170	175	
Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	180	185	190	
Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	195	200	205	
Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	210	215	220	
Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	225	230	235	240
Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	245	250	255	
Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	260	265	270	
Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	275	280	285	
Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	290	295	300	
Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	305	310	315	320
Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	325	330	335	
Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	340	345	350	
Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	355	360	365	

Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu
 370 375 380
 Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr
 385 390 395 400
 Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His
 405 410 415
 Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln
 420 425 430
 Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn
 435 440 445
 Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 450 455 460

<210> 28

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 28

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu
20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp
130 135 140

Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	
145					150					155					160	
Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	
				165				170						175		
Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	
			180					185					190			
Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	
		195					200					205				
Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	
	210					215					220					
Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	
225					230					235					240	
Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	
				245					250					255		
Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	
			260					265						270		
Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	
		275					280					285				
Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	
	290					295					300					
Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	
305					310					315					320	
Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	
				325					330					335		
Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	
			340					345					350			
Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	
		355					360					365				
Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	
	370					375					380					
Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	
385					390					395					400	
Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	
				405					410					415		
Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	
			420					425					430			
Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	
		435					440					445				

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
 450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 29
 <211> 473
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 29
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15
 Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr
 20 25 30
 Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile
 35 40 45
 Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
 50 55 60
 Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu
 65 70 75 80
 Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn
 85 90 95
 Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val
 100 105 110
 Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
 115 120 125
 Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg
 130 135 140
 Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe
 145 150 155 160
 Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp
 165 170 175
 Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
 180 185 190
 Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala
 195 200 205
 Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn
 210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly
 225 230 235 240
 Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp
 245 250 255
 Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn
 260 265 270
 Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val
 275 280 285
 Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met
 290 295 300
 Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln
 305 310 315 320
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro
 325 330 335
 Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly
 340 345 350
 Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn
 355 360 365
 Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys
 370 375 380
 Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly
 385 390 395 400
 Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile
 405 410 415
 Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu
 420 425 430
 His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
 435 440 445
 Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
 450 455 460
 Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

33

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
305 310 315 320

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
325 330 335

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
50 55